



SEQUENCE LISTING

<110> ~~Chang, Yung-Fu~~ Research Foundation
Chang, Yung-Fu

<120> Ehrlichia canis Genes for Vaccine Development

<130> CRF 2322 CIP

<160> 13

<170> PatentIn version 3.1

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ttctatccag 240

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cgcgcagaaa 300

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gaataaactt 540

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gcaaaataat 600

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gataccatag 2160

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taatagcaga 2700

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caacagaaat 2760

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atgaattagt 3540

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cttgacaaaa 4080

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taatgtggct 5100

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caaaaaacaa 5160

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<223> Protein translated from nucleotides 12 through 533
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Ile Ile
1 5 10
15

cta tct atg ata tgt tta gtg tac gct tct gta cca cta tat
agt ata 96
Leu Ser Met Ile Cys Leu Val Tyr Ala Ser Val Pro Leu Tyr
Ser Ile
20 25 30

ttt tgt aaa gta aca ggt tat gga ggt aca gta aga aca agt
aat ata 144
Phe Cys Lys Val Thr Gly Tyr Gly Gly Thr Val Arg Thr Ser
Asn Ile
35 40 45

tca aat tct aaa ata ggt aac act att att aaa gtc aga ttt
aat gca 192
Ser Asn Ser Lys Ile Gly Asn Thr Ile Ile Lys Val Arg Phe
Asn Ala
50 55 60

gat ata cac aaa caa ctg cca tgg aaa ttc tat cca gaa gta

tct cat 240
 Asp Ile His Lys Gln Leu Pro Trp Lys Phe Tyr Pro Glu Val
 Ser His
 65 70 75

80

gta ttt gta aaa cca gga gaa caa aaa ttg att ttc tac cgc
 gca gaa 288
 Val Phe Val Lys Pro Gly Glu Gln Lys Leu Ile Phe Tyr Arg
 Ala Glu

85

90

95

aat cta ctt gat gag gac act tca gga atg gct gta tat aat
 gtt aca 336
 Asn Leu Leu Asp Glu Asp Thr Ser Gly Met Ala Val Tyr Asn
 Val Thr

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105

110

cca cat aaa gta gga aaa tat ttt aat aag gta gct tgt ttt
 tgt ttc 384
 Pro His Lys Val Gly Lys Tyr Phe Asn Lys Val Ala Cys Phe
 Cys Phe

115

120

125

acc aaa caa aca tta tac cct cat caa aaa act ata atg cca
 gta tca 432
 Thr Lys Gln Thr Leu Tyr Pro His Gln Lys Thr Ile Met Pro
 Val Ser

130

135

140

ttt ttt ata gat cca gcc ata gaa aca gat cct gaa act gct
 gac gta 480
 Phe Phe Ile Asp Pro Ala Ile Glu Thr Asp Pro Glu Thr Ala
 Asp Val

145

150

155

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 Ser Ile
 20 25 30

Phe Cys Lys Val Thr Gly Tyr Gly Gly Thr Val Arg Thr Ser
 Asn Ile
 35 40 45

Ser Asn Ser Lys Ile Gly Asn Thr Ile Ile Lys Val Arg Phe
 Asn Ala
 50 55 60

Asp Ile His Lys Gln Leu Pro Trp Lys Phe Tyr Pro Glu Val
 Ser His
 65 70 75
 80

Val Phe Val Lys Pro Gly Glu Gln Lys Leu Ile Phe Tyr Arg
 Ala Glu
 85 90
 95

Asn Leu Leu Asp Glu Asp Thr Ser Gly Met Ala Val Tyr Asn
 Val Thr
 100 105 110

Pro His Lys Val Gly Lys Tyr Phe Asn Lys Val Ala Cys Phe
Cys Phe

115

120

125

Thr Lys Gln Thr Leu Tyr Pro His Gln Lys Thr Ile Met Pro
Val Ser

130

135

140

Phe Phe Ile Asp Pro Ala Ile Glu Thr Asp Pro Glu Thr Ala
Asp Val

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160

Lys Leu Ile Thr Leu Ser Tyr Val Phe Phe Lys Tyr Lys Glu
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Ile Ala

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5

10

15

aat cat gct tta tcc ttt aac att aaa gtt aca cat gaa aaa
tta gat 96

Asn His Ala Leu Ser Phe Asn Ile Lys Val Thr His Glu Lys
Leu Asp

20

25

30

aat gga atg gaa gta tac gtg att cca aat cat cgc gca cca
gca gtc 144
Asn Gly Met Glu Val Tyr Val Ile Pro Asn His Arg Ala Pro
Ala Val
35 40 45

atg cac atg gta tta tac aaa gtc ggt gga act gat gat cca
gta gga 192
Met His Met Val Leu Tyr Lys Val Gly Gly Thr Asp Asp Pro
Val Gly
50 55 60

tac tct gga tta gca cat ttt ttt gaa cac tta atg ttt agt
gga aca 240
Tyr Ser Gly Leu Ala His Phe Phe Glu His Leu Met Phe Ser
Gly Thr
65 70 75
80

gaa aaa ttt cct aat ctc atc agc aca ctt agt aat ata ggc
gga aat 288
Glu Lys Phe Pro Asn Leu Ile Ser Thr Leu Ser Asn Ile Gly
Gly Asn
85 90
95

ttc aat gca agc aca tct caa ttt tgt act ata tac tac gaa
tta ata 336
Phe Asn Ala Ser Thr Ser Gln Phe Cys Thr Ile Tyr Tyr Glu
Leu Ile
100 105 110

cca aaa caa tat tta tct ctt gca atg gat att gaa tca gac
aga atg 384
Pro Lys Gln Tyr Leu Ser Leu Ala Met Asp Ile Glu Ser Asp
Arg Met
115 120 125

cag aat ttt aag gtt acc gac aaa gca tta ata aga gaa caa
aag gta 432
Gln Asn Phe Lys Val Thr Asp Lys Ala Leu Ile Arg Glu Gln

Lys Val

130

135

140

gtc tta gaa gaa aga aaa atg aga gtt gaa agc caa gca aaa

aac ata 480

Val Leu Glu Glu Arg Lys Met Arg Val Glu Ser Gln Ala Lys

Asn Ile

145

150

155

160

cta gaa gaa gaa atg gaa aat gca ttt tat tac aat gga tat

ggc aga 528

Leu Glu Glu Glu Met Glu Asn Ala Phe Tyr Tyr Asn Gly Tyr

Gly Arg

165

170

175

cca gta gta gga tgg gaa cat gaa att agc aac tac aac aaa

gaa gtt 576

Pro Val Val Gly Trp Glu His Glu Ile Ser Asn Tyr Asn Lys

Glu Val

180

185

190

gct gaa gcc ttt cat aag cta cat tat agt cct aat aat gct

ata tta 624

Ala Glu Ala Phe His Lys Leu His Tyr Ser Pro Asn Asn Ala

Ile Leu

195

200

205

att gta act gga gat gca gat cca caa gaa gta atc aca ctt

gca aaa 672

Ile Val Thr Gly Asp Ala Asp Pro Gln Glu Val Ile Thr Leu

Ala Lys

210

215

220

caa tac tat ggg aaa ata cca tct aat aat aag aaa cct tca

agt caa 720

Gln Tyr Tyr Gly Lys Ile Pro Ser Asn Asn Lys Lys Pro Ser

Ser Gln

225

230

235

240

gtt agg gta gaa cca ccg cat aaa aca aat atg act tta aca

tta aaa 768

Val Arg Val Glu Pro Pro His Lys Thr Asn Met Thr Leu Thr
Leu Lys

245

250

255

gac agt tca gta gaa atc cca gaa ctg ttt tta atg tat caa
ata cca 816
Asp Ser Ser Val Glu Ile Pro Glu Leu Phe Leu Met Tyr Gln
Ile Pro

260

265

270

aat ggt att acc aat aaa aac tac ata ctt aac atg atg tta
gca gaa 864
Asn Gly Ile Thr Asn Lys Asn Tyr Ile Leu Asn Met Met Leu
Ala Glu

275

280

285

ata ctc ggt agt ggt aaa ttc agc ctg ctt tac aat gat ttg
gta att 912
Ile Leu Gly Ser Gly Lys Phe Ser Leu Leu Tyr Asn Asp Leu
Val Ile
290 295 300

aac aat cca ata gtt aca tcg ata aaa aca gat tat aat tac
tta act 960
Asn Asn Pro Ile Val Thr Ser Ile Lys Thr Asp Tyr Asn Tyr
Leu Thr
305 310 315
320

gac agc gat aat tac ctt tcc att gaa gct ata cct aaa aac
ggg atc 1008
Asp Ser Asp Asn Tyr Leu Ser Ile Glu Ala Ile Pro Lys Asn
Gly Ile
325 330

335

tct aca gaa gct gta gaa caa gaa att cat aaa tgt ata aat
aat tat 1056
Ser Thr Glu Ala Val Glu Gln Glu Ile His Lys Cys Ile Asn
Asn Tyr
340 345 350

tta gaa aat gga att tca gca gaa tat tta gaa agt gca aag

tat aaa 1104
 Leu Glu Asn Gly Ile Ser Ala Glu Tyr Leu Glu Ser Ala Lys
 Tyr Lys
 355 360 365

gta aaa gca cat tta act tat gca ttt gac gga cta act ttc
 ata tca 1152
 Val Lys Ala His Leu Thr Tyr Ala Phe Asp Gly Leu Thr Phe
 Ile Ser
 370 375 380

tat ttt tat ggc atg cat cta ata cta gga gta ccg cta tca
 gaa atc 1200
 Tyr Phe Tyr Gly Met His Leu Ile Leu Gly Val Pro Leu Ser
 Glu Ile
 385 390 395
 400

agt aat att tac gat acc ata gac aaa gta agt atc caa gat
 gtt aac 1248
 Ser Asn Ile Tyr Asp Thr Ile Asp Lys Val Ser Ile Gln Asp
 Val Asn
 405 410
 415

tcc gct atg gaa aat atc ttt caa aac aat ata aga tta acc
 ggg cat 1296
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 420 425 430

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 Leu Asp
 20 25 30

Asn Gly Met Glu Val Tyr Val Ile Pro Asn His Arg Ala Pro
 Ala Val
 35 40 45

Met His Met Val Leu Tyr Lys Val Gly Gly Thr Asp Asp Pro
 Val Gly
 50 55 60

Tyr Ser Gly Leu Ala His Phe Phe Glu His Leu Met Phe Ser
 Gly Thr
 65 70 75
 80

Glu Lys Phe Pro Asn Leu Ile Ser Thr Leu Ser Asn Ile Gly
 Gly Asn
 85 90
 95

Phe Asn Ala Ser Thr Ser Gln Phe Cys Thr Ile Tyr Tyr Glu
 Leu Ile
 100 105 110

Pro Lys Gln Tyr Leu Ser Leu Ala Met Asp Ile Glu Ser Asp
 Arg Met
 115 120 125

Gln Asn Phe Lys Val Thr Asp Lys Ala Leu Ile Arg Glu Gln
 Lys Val
 130 135 140

Val Leu Glu Glu Arg Lys Met Arg Val Glu Ser Gln Ala Lys
 Asn Ile
 145 150 155
 160

Leu Glu Glu Glu Met Glu Asn Ala Phe Tyr Tyr Asn Gly Tyr
 Gly Arg
 165 170
 175

Pro Val Val Gly Trp Glu His Glu Ile Ser Asn Tyr Asn Lys
 Glu Val
 180 185 190

Ala Glu Ala Phe His Lys Leu His Tyr Ser Pro Asn Asn Ala
 Ile Leu
 195 200 205

Ile Val Thr Gly Asp Ala Asp Pro Gln Glu Val Ile Thr Leu
 Ala Lys
 210 215 220

Gln Tyr Tyr Gly Lys Ile Pro Ser Asn Asn Lys Lys Pro Ser
 Ser Gln
 225 230 235
 240

Val Arg Val Glu Pro Pro His Lys Thr Asn Met Thr Leu Thr
 Leu Lys
 245 250
 255

Asp Ser Ser Val Glu Ile Pro Glu Leu Phe Leu Met Tyr Gln
 Ile Pro
 260 265 270

Asn Gly Ile Thr Asn Lys Asn Tyr Ile Leu Asn Met Met Leu
 Ala Glu
 275 280 285

Ile Leu Gly Ser Gly Lys Phe Ser Leu Leu Tyr Asn Asp Leu
 Val Ile
 290 295 300

Asn Asn Pro Ile Val Thr Ser Ile Lys Thr Asp Tyr Asn Tyr
 Leu Thr
 305 310 315
 320

Asp Ser Asp Asn Tyr Leu Ser Ile Glu Ala Ile Pro Lys Asn
 Gly Ile
 325 330
 335

Ser Thr Glu Ala Val Glu Gln Glu Ile His Lys Cys Ile Asn
 Asn Tyr
 340 345 350

Leu Glu Asn Gly Ile Ser Ala Glu Tyr Leu Glu Ser Ala Lys
 Tyr Lys
 355 360 365

Val Lys Ala His Leu Thr Tyr Ala Phe Asp Gly Leu Thr Phe
 Ile Ser
 370 375 380

Tyr Phe Tyr Gly Met His Leu Ile Leu Gly Val Pro Leu Ser
 Glu Ile
 385 390 395
 400

Ser Asn Ile Tyr Asp Thr Ile Asp Lys Val Ser Ile Gln Asp
 Val Asn
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 415

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 Gly His
 420 425 430

Leu Leu Pro Asn Gly Glu
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 <223> Protein translated from nucleotides 2,258 through
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 Ser Phe
 1 5 10
 15

aat aca tat gca aat gat ctc aat att aac ata aaa gaa gct
 aca act 96
 Asn Thr Tyr Ala Asn Asp Leu Asn Ile Asn Ile Lys Glu Ala
 Thr Thr
 20 25 30

aaa aat aaa ata cac tat cta tat gtt gaa cat cat aac cta
 cca aca 144
 Lys Asn Lys Ile His Tyr Leu Tyr Val Glu His His Asn Leu
 Pro Thr

35

40

45

att tcc tta aaa ttt gca ttc aag aaa gca gga tac gct tat
 gat gcc 192
 Ile Ser Leu Lys Phe Ala Phe Lys Lys Ala Gly Tyr Ala Tyr
 Asp Ala
 50 55 60

ttt gat aag caa gga ctt gca tac ttt aca tca aaa ata tta
 aac gaa 240
 Phe Asp Lys Gln Gly Leu Ala Tyr Phe Thr Ser Lys Ile Leu
 Asn Glu
 65 70 75
 80

gga tca aaa aac aac tat gct ctc agt ttt gca caa caa tta
 gaa ggc 288
 Gly Ser Lys Asn Asn Tyr Ala Leu Ser Phe Ala Gln Gln Leu
 Glu Gly
 85 90
 95

aaa ggt ata gac tta aaa ttt gat ata gac cta gac aat ttt
 tat ata 336
 Lys Gly Ile Asp Leu Lys Phe Asp Ile Asp Leu Asp Asn Phe
 Tyr Ile
 100 105 110

tca tta aaa acc tta tca gaa aac ttt gaa gaa gcc cta gtt
 tta ctc 384
 Ser Leu Lys Thr Leu Ser Glu Asn Phe Glu Glu Ala Leu Val
 Leu Leu
 115 120 125

agt gat tgc ata ttc aac acc gtc aca gat caa gaa ata ttc
 aat aga 432
 Ser Asp Cys Ile Phe Asn Thr Val Thr Asp Gln Glu Ile Phe
 Asn Arg

130	135	140
ata ata gca gaa cag att gca cat gtt aaa tca tta tat tct		
gct cct 480		
Ile Ile Ala Glu Gln Ile Ala His Val Lys Ser Leu Tyr Ser		
Ala Pro		
145	150	155
160		
gaa ttt ata gct aca aca gaa atg aat cac gct ata ttc aaa		
ggg cac 528		
Glu Phe Ile Ala Thr Thr Glu Met Asn His Ala Ile Phe Lys		
Gly His		
	165	170
175		
cca tat tct aac aaa gtt tac ggg aca tta aat aca atc aat		
aat atc 576		
Pro Tyr Ser Asn Lys Val Tyr Gly Thr Leu Asn Thr Ile Asn		
Asn Ile		
	180	185 190
aac cag gaa gac gtt gca tta tat ata aaa aat agt ttt gac		
aag gaa 624		
Asn Gln Glu Asp Val Ala Leu Tyr Ile Lys Asn Ser Phe Asp		
Lys Glu		
195	200	205
caa atc gtt atc agc gca gca gga gat gta gat cca aca cag		
cta tca 672		
Gln Ile Val Ile Ser Ala Ala Gly Asp Val Asp Pro Thr Gln		
Leu Ser		
210	215	220
aat tta cta gat aaa tat att ctt tcc aaa ttg cca tct ggt		
aat aac 720		
Asn Leu Leu Asp Lys Tyr Ile Leu Ser Lys Leu Pro Ser Gly		
Asn Asn		
225	230	235
240		
aaa aat acc ata cca gat acg act gtt aat aga gaa gac aca		
tta tta 768		
Lys Asn Thr Ile Pro Asp Thr Thr Val Asn Arg Glu Asp Thr		

Leu Leu

245

250

255

tat gta cag aga gat gta cca caa agt gtc ata atg ttt gct
aca gac 816
Tyr Val Gln Arg Asp Val Pro Gln Ser Val Ile Met Phe Ala
Thr Asp
260 265 270

aca gta cca tat cac agc aaa gac tat cat gca tca aac ttg
ttc aat 864
Thr Val Pro Tyr His Ser Lys Asp Tyr His Ala Ser Asn Leu
Phe Asn
275 280 285

act atg cta ggc gga tta agt ctc aat tca ata tta atg ata
gaa tta 912
Thr Met Leu Gly Gly Leu Ser Leu Asn Ser Ile Leu Met Ile
Glu Leu
290 295 300

aga gac aag tta gga tta aca tac cat agt agc agt tca cta
tct aac 960
Arg Asp Lys Leu Gly Leu Thr Tyr His Ser Ser Ser Ser Leu
Ser Asn
305 310 315
320

atg aat cat agt aat gtg cta ttt ggt aca ata ttc act gat
aat acc 1008
Met Asn His Ser Asn Val Leu Phe Gly Thr Ile Phe Thr Asp
Asn Thr
325 330
335

aca gta aca aaa tgt ata tcc gtc tta aca gat att ata gag
cac att 1056
Thr Val Thr Lys Cys Ile Ser Val Leu Thr Asp Ile Ile Glu
His Ile
340 345 350

aaa aag tat gga gtt gat gaa gac act ttt gca att gca aaa
tct agt 1104

Lys Lys Tyr Gly Val Asp Glu Asp Thr Phe Ala Ile Ala Lys
 Ser Ser
 355 360 365

att acc aac tct ttt att tta tct atg tta aat aac aat aat
 gtt agt 1152
 Ile Thr Asn Ser Phe Ile Leu Ser Met Leu Asn Asn Asn Asn
 Val Ser
 370 375 380

gag ata ttg tta agc tta caa tta cac gat cta gat ccg agt
 tat att 1200
 Glu Ile Leu Leu Ser Leu Gln Leu His Asp Leu Asp Pro Ser
 Tyr Ile
 385 390 395
 400

aat aaa tac aat tct tac tac aaa gca ata aca ata gaa gaa
 gta aat 1248
 Asn Lys Tyr Asn Ser Tyr Tyr Lys Ala Ile Thr Ile Glu Glu
 Val Asn
 405 410
 415

aaa att gcc aag aaa att tta tct aat gaa tta gta ata att
 gaa gta 1296
 Lys Ile Ala Lys Lys Ile Leu Ser Asn Glu Leu Val Ile Ile
 Glu Val
 420 425 430

gga aaa aac aat aac ata aat ggc aaa caa ata gat gct aaa
 aaa cac 1344
 Gly Lys Asn Asn Asn Ile Asn Gly Lys Gln Ile Asp Ala Lys
 Lys His
 435 440 445

ata ctt ggt
 1353
 Ile Leu Gly
 450

<210> 7
 <211> 451
 <212> PRT
 <213> Ehrlichia canis

<400> 7

Met Arg Asn Ile Leu Cys Tyr Thr Leu Ile Leu Ile Phe Phe
 Ser Phe
 1 5 10
 15

Asn Thr Tyr Ala Asn Asp Leu Asn Ile Asn Ile Lys Glu Ala
 Thr Thr
 20 25 30

Lys Asn Lys Ile His Tyr Leu Tyr Val Glu His His Asn Leu
 Pro Thr
 35 40 45

Ile Ser Leu Lys Phe Ala Phe Lys Lys Ala Gly Tyr Ala Tyr
 Asp Ala
 50 55 60

Phe Asp Lys Gln Gly Leu Ala Tyr Phe Thr Ser Lys Ile Leu
 Asn Glu
 65 70 75
 80

Gly Ser Lys Asn Asn Tyr Ala Leu Ser Phe Ala Gln Gln Leu
 Glu Gly
 85 90
 95

Lys Gly Ile Asp Leu Lys Phe Asp Ile Asp Leu Asp Asn Phe
 Tyr Ile
 100 105 110

Ser Leu Lys Thr Leu Ser Glu Asn Phe Glu Glu Ala Leu Val
 Leu Leu
 115 120 125

Ser Asp Cys Ile Phe Asn Thr Val Thr Asp Gln Glu Ile Phe
 Asn Arg
 130 135 140

Ile Ile Ala Glu Gln Ile Ala His Val Lys Ser Leu Tyr Ser
 Ala Pro
 145 150 155
 160

Glu Phe Ile Ala Thr Thr Glu Met Asn His Ala Ile Phe Lys
 Gly His
 165 170
 175

Pro Tyr Ser Asn Lys Val Tyr Gly Thr Leu Asn Thr Ile Asn
 Asn Ile
 180 185 190

Asn Gln Glu Asp Val Ala Leu Tyr Ile Lys Asn Ser Phe Asp
 Lys Glu
 195 200 205

Gln Ile Val Ile Ser Ala Ala Gly Asp Val Asp Pro Thr Gln
 Leu Ser
 210 215 220

Asn Leu Leu Asp Lys Tyr Ile Leu Ser Lys Leu Pro Ser Gly
 Asn Asn
 225 230 235
 240

Lys Asn Thr Ile Pro Asp Thr Thr Val Asn Arg Glu Asp Thr
Leu Leu

245

250

255

Tyr Val Gln Arg Asp Val Pro Gln Ser Val Ile Met Phe Ala
Thr Asp

260

265

270

Thr Val Pro Tyr His Ser Lys Asp Tyr His Ala Ser Asn Leu
Phe Asn

275

280

285

Thr Met Leu Gly Gly Leu Ser Leu Asn Ser Ile Leu Met Ile
Glu Leu

290

295

300

Arg Asp Lys Leu Gly Leu Thr Tyr His Ser Ser Ser Ser Leu
Ser Asn

305

310

315

320

Met Asn His Ser Asn Val Leu Phe Gly Thr Ile Phe Thr Asp
Asn Thr

325

330

335

Thr Val Thr Lys Cys Ile Ser Val Leu Thr Asp Ile Ile Glu
His Ile

340

345

350

Lys Lys Tyr Gly Val Asp Glu Asp Thr Phe Ala Ile Ala Lys
Ser Ser

355

360

365

Ile Thr Asn Ser Phe Ile Leu Ser Met Leu Asn Asn Asn Asn
Val Ser
370 375 380

Glu Ile Leu Leu Ser Leu Gln Leu His Asp Leu Asp Pro Ser
Tyr Ile
385 390 395
400

Asn Lys Tyr Asn Ser Tyr Tyr Lys Ala Ile Thr Ile Glu Glu
Val Asn
405 410
415

Lys Ile Ala Lys Lys Ile Leu Ser Asn Glu Leu Val Ile Ile
Glu Val
420 425 430

Gly Lys Asn Asn Asn Ile Asn Gly Lys Gln Ile Asp Ala Lys
Lys His
435 440 445

Ile Leu Gly
450

<210> 8
<211> 663
<212> DNA
<213> Ehrlichia canis

<220>
<221> CDS
<222> (1)..(663)
<223> Protein translated from nucleotides 4,132 through
4,794 (mmpA).

<400> 8

atg aaa gct cat agc aca agt ata cgg aac ttt cag cct tta
 gaa aga 48
 Met Lys Ala His Ser Thr Ser Ile Arg Asn Phe Gln Pro Leu
 Glu Arg

1 5 10
 15

gct gct ata atc att gca gtg tta ggt tta gct gca ttc ttg
 ttt gct 96
 Ala Ala Ile Ile Ile Ala Val Leu Gly Leu Ala Ala Phe Leu
 Phe Ala

20 25 30

gct gct gcc tgc agt gat cgt ttc caa aga ttg caa tta aca
 aat cca 144
 Ala Ala Ala Cys Ser Asp Arg Phe Gln Arg Leu Gln Leu Thr
 Asn Pro

35 40 45

ttt gta ata gca gga atg gtt ggc ctt gca gtt ctt tta gtt
 gct tcc 192
 Phe Val Ile Ala Gly Met Val Gly Leu Ala Val Leu Leu Val
 Ala Ser

50 55 60

tta aca gca gca tta agt ata tgc tta act aaa agt aag caa
 gtc aca 240
 Leu Thr Ala Ala Leu Ser Ile Cys Leu Thr Lys Ser Lys Gln
 Val Thr

65 70 75

80

caa cat gct att aga cat cgc ttt gga tac gag tca agc act
 tct tct 288
 Gln His Ala Ile Arg His Arg Phe Gly Tyr Glu Ser Ser Thr
 Ser Ser

85 90

95

tct gta ctg ctt gca ata tca ata att tct tta tta ctt gct
 gca gca 336
 Ser Val Leu Leu Ala Ile Ser Ile Ile Ser Leu Leu Leu Ala
 Ala Ala

100 105 110

ttt tgt gga aag ata atg ggt aat gac aac cca gat cta ttc
 ttt agc 384
 Phe Cys Gly Lys Ile Met Gly Asn Asp Asn Pro Asp Leu Phe
 Phe Ser

115

120

125

aag atg caa gaa ctc tcc aat cca ctt gtt gtt gca gct att
 gta gcc 432
 Lys Met Gln Glu Leu Ser Asn Pro Leu Val Val Ala Ala Ile
 Val Ala

130

135

140

gtt tct gtt ttc cta ctc tca ttc gta atg tat gct gca aag
 aac att 480
 Val Ser Val Phe Leu Leu Ser Phe Val Met Tyr Ala Ala Lys
 Asn Ile

145

150

155

160

ata agt cca gat aaa caa act cac gtt att ata tta tct aat
 caa caa 528
 Ile Ser Pro Asp Lys Gln Thr His Val Ile Ile Leu Ser Asn
 Gln Gln

165

170

175

act ata gaa gaa gca aaa gta gat caa gga atg aat att ttg
 tca gca 576
 Thr Ile Glu Glu Ala Lys Val Asp Gln Gly Met Asn Ile Leu
 Ser Ala

180

185

190

gta ctc cca gca gct ggc att gac atc atg act ata gct tct
 tgt gac 624
 Val Leu Pro Ala Ala Gly Ile Asp Ile Met Thr Ile Ala Ser
 Cys Asp

195

200

205

att tta gca gtg agc agc cgg gga tcc tct cag cat caa
 663
 Ile Leu Ala Val Ser Ser Arg Gly Ser Ser Gln His Gln

210

215

220

<210> 9
 <211> 221
 <212> PRT
 <213> Ehrlichia canis

<400> 9

Met Lys Ala His Ser Thr Ser Ile Arg Asn Phe Gln Pro Leu
 Glu Arg
 1 5 10
 15

Ala Ala Ile Ile Ile Ala Val Leu Gly Leu Ala Ala Phe Leu
 Phe Ala
 - - -20 - - - 25 - - - 30

Ala Ala Ala Cys Ser Asp Arg Phe Gln Arg Leu Gln Leu Thr
 Asn Pro
 35 40 45

Phe Val Ile Ala Gly Met Val Gly Leu Ala Val Leu Leu Val
 Ala Ser
 50 55 60

Leu Thr Ala Ala Leu Ser Ile Cys Leu Thr Lys Ser Lys Gln
 Val Thr
 65 70 75
 80

Gln His Ala Ile Arg His Arg Phe Gly Tyr Glu Ser Ser Thr
 Ser Ser
 85 90
 95

Ser Val Leu Leu Ala Ile Ser Ile Ile Ser Leu Leu Leu Ala
 Ala Ala

100

105

110

Phe Cys Gly Lys Ile Met Gly Asn Asp Asn Pro Asp Leu Phe
Phe Ser

115

120

125

Lys Met Gln Glu Leu Ser Asn Pro Leu Val Val Ala Ala Ile
Val Ala

130

135

140

Val Ser Val Phe Leu Leu Ser Phe Val Met Tyr Ala Ala Lys
Asn Ile

145

150

155

160

Ile Ser Pro Asp Lys Gln Thr His Val Ile Ile Leu Ser Asn
Gln Gln

165

170

175

Thr Ile Glu Glu Ala Lys Val Asp Gln Gly Met Asn Ile Leu
Ser Ala

180

185

190

Val Leu Pro Ala Ala Gly Ile Asp Ile Met Thr Ile Ala Ser
Cys Asp

195

200

205

Ile Leu Ala Val Ser Ser Arg Gly Ser Ser Gln His Gln
210 215 220

<210> 10

<211> 417

<212> DNA

<213> Ehrlichia canis

<220>

<221> CDS

<222> (1)..(417)

<223> Protein translated from complementary sequence
 derived from nucle
 otides 4,883 through 5,299 (partial lipoprotein
 signal peptidase
 homolog).

<400> 10

gat cag gta agt aaa tgg tat gta gta aat ttg ata gga gat

aaa ggt 48

Asp Gln Val Ser Lys Trp Tyr Val Val Asn Leu Ile Gly Asp

Lys Gly

1

5

10

15

gta ata gag ata tta agc ttc ttg cgc ttt act aca gtg tgg

aat cct 96

Val Ile Glu Ile Leu Ser Phe Leu Arg Phe Thr Thr Val Trp

Asn Pro

20

25

30

gga att agt ttt ggt ata tta aat aac ttt gaa tat agt aat

gtt gtt 144

Gly Ile Ser Phe Gly Ile Leu Asn Asn Phe Glu Tyr Ser Asn

Val Val

35

40

45

ttt tgt agt atc tcg att ttg att act tgt gtt tta tgc tac

tta ttt 192

Phe Cys Ser Ile Ser Ile Leu Ile Thr Cys Val Leu Cys Tyr

Leu Phe

50

55

60

ata gta cag cca cat tat aga tta cct ctt gta atc att att

ggg ggg 240

Ile Val Gln Pro His Tyr Arg Leu Pro Leu Val Ile Ile Ile

Gly Gly

65

70

75

80

tca ata gga aat atc ata gat aga ata aga tat ggt gct gtc

tat gat 288
 Ser Ile Gly Asn Ile Ile Asp Arg Ile Arg Tyr Gly Ala Val
 Tyr Asp

85

90

95

ttt ata gat ttt tat atc aat aac tta cat tgg cct gta ttc
 aac ctg 336
 Phe Ile Asp Phe Tyr Ile Asn Asn Leu His Trp Pro Val Phe
 Asn Leu

100

105

110

gcg gat tct ttt ata ttt tta ggt ata gta ata ata atg gca
 aag agt 384
 Ala Asp Ser Phe Ile Phe Leu Gly Ile Val Ile Ile Met Ala
 Lys Ser

115

120

125

aat aac cac atg aaa caa att aac tgt aac tcc
 417

Asn Asn His Met Lys Gln Ile Asn Cys Asn Ser

130

135

<210> 11
 <211> 139
 <212> PRT
 <213> Ehrlichia canis

<400> 11

Asp Gln Val Ser Lys Trp Tyr Val Val Asn Leu Ile Gly Asp
 Lys Gly

1

5

10

15

Val Ile Glu Ile Leu Ser Phe Leu Arg Phe Thr Thr Val Trp
 Asn Pro

20

25

30

Gly Ile Ser Phe Gly Ile Leu Asn Asn Phe Glu Tyr Ser Asn

Val Val
35 40 45

Phe Cys Ser Ile Ser Ile Leu Ile Thr Cys Val Leu Cys Tyr
Leu Phe
50 55 60

Ile Val Gln Pro His Tyr Arg Leu Pro Leu Val Ile Ile Ile
Gly Gly
65 70 75
80

Ser Ile Gly Asn Ile Ile Asp Arg Ile Arg Tyr Gly Ala Val
Tyr Asp
85 90
95

Phe Ile Asp Phe Tyr Ile Asn Asn Leu His Trp Pro Val Phe
Asn Leu
100 105 110

Ala Asp Ser Phe Ile Phe Leu Gly Ile Val Ile Ile Met Ala
Lys Ser
115 120 125

Asn Asn His Met Lys Gln Ile Asn Cys Asn Ser
130 135

<210> 12
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artifical Sequence: oligonucleotide
<400> 12

aggcttggtc agggatgaaga agaattccaac gacaaaagct t
41

<210> 13

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 13

aagcttttgt cgttggattc ttcttcaccc tgaacttgcc a
41